Please amend the application as follows:

In the Specification

Please replace the paragraph at page 1, line 13 through page 2, line 16, with the following paragraph:

Lyme disease begins at the site of a tick bite, producing a primary infection with spread of the organism to secondary sites occurring early in the course of infection. Lyme disease is a progressive multi-system disorder and is the most common vector-borne disease in both North America and Europe. This disease was first described as a focus of pediatric arthritis patients in Old Lyme, CT (Steere, A.C., *et al., Arth. Rheum.,* 20:17 (1977)). The association of this syndrome with the bite of the deer tick, *Ixodes scapularis*, led to the identification of the spirochete *Borrelia burgdorferi* as the causative agent (Burgdorfer, W., *et al., Science,* 216:1317-1319 (1982)). As culture isolation of the bacterium from clinical and field samples became more efficient, Baranton and colleagues described three pathogenic genospecies, *B. burgdorferi sensu stricto* (*B. burgdorferi* or *B.b.s.s.*), *B. afzelii*, and *B. garinii* (Baraton, G., *et al., Int. J. Syst. Bacteriol.,* 42:378-383 (1992)). These are members of a species complex, *B. burgdorferi* sensu lato, which consists of at least 10 different genospecies (Piken, R.N., *et al., J. Invest. Dermatol.,* 110:211-214 (1998); Postic, D., *et al., Int. J. Syst. Bacteriol.*, 44:743-752 (1994); Valsangiacomo, C.T., *et al., Int. J. Syst. Bacteriol.*, 47:1-10 (1997)). *B. burgdorferi*, *B. afzelii* and *B. garinii* are thought to be pathogenic and all are found in Europe, but in North America, *B. burgdorferi* is the only pathogenic genospecies found. Each of these three genospecies is associated with distinct clinical manifestations (Van Dam, A. P. *et al., Clin. Infect. Dis.,* 17:708-717 (1993)). This implies that differences in genospecies may play an important role in the wide array of clinical manifestations observed in Lyme Disease.

Please replace the paragraph at page 10, lines 18-26, with the following paragraph:

There is evidence that *ospC* has been transferred between strains and even between genospecies (Wang I-N, *et al., Genetics, 151*:15-30 (1998)). This is not true of *Borrelia* chromosomal genes (Dykhuizen, D.E., *et al., Proc. Natl. Acad. Sci.*, 30:10163-10167 (1999); Maynard Smith, J. and Smith, N.H., *Mol. Biol. Evol.*, 15:590-599 (1998)). However, *ospA* and *ospC* alleles in *B. burgdorferi* sensu stricto are almost completely linked (Wang I-N, *et al., Genetics,* 151:15-30 (1999)). This suggests that once an *ospC* allele has been transferred into a particular background, there is little or no selection for another similar recombination event. Thus, each major *ospC* group represents a clonal population descended from a single recombination.

B2

Please replace the paragraph at page 43, lines 1-25, with the following paragraph:

TABLE VII

OspC Polypeptides and Chimeric Polypeptides of the Present Invention

POLYPEPTIDE	SEQ ID NO.:(DNA)	(POLYPEPTIDES)
[1]unlip OspC kkp(55-621*)	45	46
unlip OspC PKO	47	48
unlip OspC TRO	49	50
[2]unlip OspC-55B31/ 58PKO/56TRO	51	52
unlip OspC1-TRO	53	54
unlip OspC-TRO	55	56
[3]Blip OspC1C10	57	58
BlipOspC12	59	60
Blip OspC1-TR0	75	76
Blip OspC2C7	65	66
Blip OspC2C10	61	62

B3